

IN THE CLAIMS

Claims 1-35 (Cancelled):

Claim 36 (New): An isolated polynucleotide

which is at least 90% identical to SEQ ID NO: 1, or to a fragment of SEQ ID NO: 1,
and

which encodes a polypeptide having the enzymatic activity of adenosyl
homocysteinase.

Claim 37 (New): The isolated polynucleotide of Claim 36, which is at least 95%
identical to SEQ ID NO: 1.

Claim 38 (New): The isolated polynucleotide of Claim 36, which encodes the
polypeptide of SEQ ID NO: 2.

Claim 39 (New): The isolated polynucleotide of Claim 36, which comprises
nucleotides 227 to 1720 of SEQ ID NO: 1.

Claim 40 (New): The isolated polynucleotide of Claim 36, further comprising at least
one promoter, ribosome binding site, regulatory region or expression cassette.

Claim 41 (New): The isolated polynucleotide of Claim 36, which is RNA.

Claim 42 (New): A vector comprising the isolated polynucleotide of Claim 36.

Claim 43 (New): A vector comprising the isolated polynucleotide of Claim 38.

Claim 44 (New): A vector comprising the isolated polynucleotide of Claim 40.

Claim 45 (New): A host cell comprising at least one copy of the isolated polynucleotide of Claim 36.

Claim 46 (New): A host cell comprising multiple copies of the isolated polynucleotide of Claim 36.

Claim 47 (New): The host cell of Claim 45, which is a coryneform bacterium.

Claim 48 (New): The host cell of Claim 45, which is *Corynebacterium glutamicum*.

Claim 49 (New): A process for making an amino acid comprising:
culturing the host cell of Claim 45 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 50 (New): The process of Claim 49, wherein said amino acid is lysine.

Claim 51 (New): The process of Claim 49, wherein said amino acid is methionine.

Claim 52 (New): The process of Claim 49, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

- the dapA gene which codes for dihydrodipicolinate synthase,
- the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- the tpi gene which codes for triose phosphate isomerase,
- the pgk gene which codes for 3-phosphoglycerate kinase,
- the zwf gene which codes for glucose 6-phosphate dehydrogenase,
- the pyc gene which codes for pyruvate carboxylase,
- the mqo gene which codes for malate-quinone oxidoreductase,
- the lysC gene which codes for a feed-back resistant aspartate kinase,
- the lysE gene which codes for lysine export,
- the hom gene which codes for homoserine dehydrogenase
- the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,
- the ilvBN gene which codes for acetohydroxy-acid synthase,
- the ilvD gene which codes for dihydroxy-acid dehydratase, or
- the zwal gene which codes for the Zwal protein; and/or

(B) reduces or eliminates the expression of one or more of the following gene(s):

- the pck gene which codes for phosphoenol pyruvate carboxykinase,
- the pgi gene which codes for glucose 6-phosphate isomerase,
- the poxB gene which codes for pyruvate oxidase or
- the zwa2 gene which codes for the Zwa2 protein.

Claim 53 (New): A host cell comprising at least one copy of the isolated polynucleotide of Claim 38.

Claim 54 (New): A host cell comprising multiple copies of the isolated polynucleotide of Claim 38.

Claim 55 (New): The host cell of Claim 53, which is a coryneform bacterium.

Claim 56 (New): The host cell of Claim 53, which is *Corynebacterium glutamicum*.

Claim 57 (New): A process for making an amino acid comprising:
culturing the host cell of Claim 53 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 58 (New): The process of Claim 57, wherein said amino acid is lysine.

Claim 59 (New): The process of Claim 57, wherein said amino acid is methionine.

Claim 60 (New): The process of Claim 57, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
the tpi gene which codes for triose phosphate isomerase,
the pgk gene which codes for 3-phosphoglycerate kinase,
the zwf gene which codes for glucose 6-phosphate dehydrogenase,
the pyc gene which codes for pyruvate carboxylase,
the mqo gene which codes for malate-quinone oxidoreductase,
the lysC gene which codes for a feed-back resistant aspartate kinase,
the lysE gene which codes for lysine export,
the hom gene which codes for homoserine dehydrogenase
the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which
codes for a feed back resistant threonine dehydratase,
the ilvBN gene which codes for acetohydroxy-acid synthase,
the ilvD gene which codes for dihydroxy-acid dehydratase, or
the zwal gene which codes for the Zwal protein; and/or

(B) reduces or eliminates the expression of one or more of the following gene(s):

the pck gene which codes for phosphoenol pyruvate carboxykinase,
the pgi gene which codes for glucose 6-phosphate isomerase,
the poxB gene which codes for pyruvate oxidase or
the zwa2 gene which codes for the Zwa2 protein.

Claim 61 (New): A host cell comprising at least one copy of the isolated polynucleotide of Claim 40.

Claim 62 (New): A host cell comprising multiple copies of the isolated polynucleotide of Claim 40.

Claim 63 (New): The host cell of Claim 61, which is a coryneform bacterium.

Claim 64 (New): The host cell of Claim 61, which is *Corynebacterium glutamicum*.

Claim 65 (New): A process for making an amino acid comprising:
culturing the host cell of Claim 61 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 66 (New): The process of Claim 65, wherein said amino acid is lysine.

Claim 67 (New): The process of Claim 65, wherein said amino acid is methionine.

Claim 68 (New): The process of Claim 65, wherein said amino acid is lysine or methionine, and said host cell is a coryneform microorganism, which compared to an unmodified starting strain:

(A) over-expresses one or more of the following genes:

the *dapA* gene which codes for dihydrodipicolinate synthase,

the *gap* gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

the *tpi* gene which codes for triose phosphate isomerase,
the *pgk* gene which codes for 3-phosphoglycerate kinase,
the *zwf* gene which codes for glucose 6-phosphate dehydrogenase,
the *pyc* gene which codes for pyruvate carboxylase,
the *mgo* gene which codes for malate-quinone oxidoreductase,
the *lysC* gene which codes for a feed-back resistant aspartate kinase,
the *lysE* gene which codes for lysine export,
the *hom* gene which codes for homoserine dehydrogenase
the *ilvA* gene which codes for threonine dehydratase or the *ilvA(Fbr)* allele which
codes for a feed back resistant threonine dehydratase,
the *ilvBN* gene which codes for acetohydroxy-acid synthase,
the *ilvD* gene which codes for dihydroxy-acid dehydratase, or
the *zwa* gene which codes for the Zwa protein; and/or

(B) reduces or eliminates the expression of one or more of the following gene(s):

the *pck* gene which codes for phosphoenol pyruvate carboxykinase,
the *pgi* gene which codes for glucose 6-phosphate isomerase,
the *poxB* gene which codes for pyruvate oxidase or
the *zwa2* gene which codes for the Zwa2 protein.

Claim 69 (New): An isolated polynucleotide that encodes a polypeptide which is at least 90% identical to SEQ ID NO: 2, which polypeptide has the biological activity of adenosyl homocysteinase.

Claim 70 (New): The isolated polynucleotide of Claim 69 that encodes a polypeptide which is at least 95% identical to SEQ ID NO: 2.

Claim 71 (New): The isolated polynucleotide of Claim 69 that encodes a polypeptide comprising SEQ ID NO: 2.

Claim 72 (New): A vector comprising the isolated polynucleotide of Claim 69.

Claim 73 (New): A host cell comprising the isolated polynucleotide of Claim 69.

Claim 74 (New): A process for producing an amino acid comprising:
culturing the host cell of Claim 73 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 75 (New): An isolated polynucleotide which hybridizes to the complement of SEQ ID NO: 1 under stringent conditions and which encodes a polypeptide having the enzymatic activity of adenosyl homocysteinase, and

wherein stringent conditions comprise washing at a temperature ranging from 50°C to 68°C in 2x SSC.

Claim 76 (New): A vector comprising the isolated polynucleotide of Claim 75.

Claim 77 (New): A host cell comprising the isolated polynucleotide of Claim 75.

Claim 78 (New): A process for producing an amino acid comprising:
culturing the host cell of Claim 77 for a time and under conditions suitable for the production of said amino acid, and
recovering said amino acid.

Claim 79 (New): An isolated polynucleotide comprising at least 30 consecutive nucleotides of SEQ ID NO:1, or at least 30 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 80 (New): The isolated polynucleotide of Claim 79 which comprises at least 40 consecutive nucleotides of SEQ ID NO: 1, or at least 40 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 81 (New): The isolated polynucleotide of Claim 79 which comprises at least 50 consecutive nucleotides of SEQ ID NO: 1, or at least 50 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 82 (New): *Escherichia coli* strain DH5 α mcr/pEC-XK99sahHalex deposited as DSM 14316.